

SEQ ID NO: 1

SEQUENCE LENGTH: 1,358

SEQUENCE TYPE: Amino acid

5 TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays L.*)

STRAIN: cultivar: Golden Cross Bantam 70

10 SEQUENCE DESCRIPTION

	5	10	15
	Met Gly Lys Glu Ala Gly Ala Ala	Glu Ser Ser Thr Val Val Leu Ala	
	20	25	30
	Val Asn Gly Lys Arg Tyr Glu Ala Ala Gly Val Ala Pro Ser Thr Ser		
15	35	40	45
	Leu Leu Glu Phe Leu Arg Thr Gln Thr Pro Val Arg Gly Pro Lys Leu		
	50	55	60
	Gly Cys Gly Glu Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys		
	65	70	75
20	Tyr Asp Pro Ala Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys		80
	85	90	95
	Leu Thr Leu Leu His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu		
	100	105	110
	Gly Ile Gly Asn Thr Arg Asp Gly Tyr His Pro Val Gln Gln Arg Leu		
25	115	120	125

Ser Gly Phe His Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys
130 135 140

Met Ser Ile Phe Ser Ala Leu Val Lys Ala Asp Asn Lys Ser Asp Arg
145 150 155 160

5 Pro Asp Pro Pro Ala Gly Phe Ser Lys Ile Thr Thr Ser Glu Ala Glu
165 170 175

Lys Ala Val Ser Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile
180 185 190

Val Asp Thr Cys Lys Ser Phe Ala Ser Asp Val Asp Leu Glu Asp Leu
10 195 200 205

Gly Leu Asn Cys Phe Trp Lys Lys Gly Glu Glu Pro Ala Glu Val Ser
210 215 220

Arg Leu Pro Gly Tyr Asn Ser Gly Ala Val Cys Thr Phe Pro Glu Phe
225 230 235 240

15 Leu Lys Ser Glu Ile Lys Ser Thr Met Lys Gln Val Asn Asp Val Pro
245 250 255

Ile Ala Ala Ser Gly Asp Gly Trp Tyr His Pro Lys Ser Ile Glu Glu
260 265 270

Leu His Arg Leu Phe Asp Ser Ser Trp Phe Asp Asp Ser Ser Val Lys
20 275 280 285

Ile Val Ala Ser Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu
290 295 300

Tyr Asp Lys Tyr Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile
305 310 315 320

25 Asn Lys Asn Asp Lys Ala Ile Glu Leu Gly Ser Val Val Ser Ile Ser

325 330 335

Lys Ala Ile Glu Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile
340 345 350

Ala Asp His Leu Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala
5 355 360 365

Thr Ile Gly Gly Asn Ile Met Met Ala Gln Arg Leu Pro Phe Glu Ser
370 375 380

Asp Val Ala Thr Val Leu Leu Ala Ala Gly Ser Thr Val Thr Val Gln
385 390 395 400

10 Val Ala Ser Lys Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Glu Gln
405 410 415

Pro Pro Cys Asp Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu
420 425 430

Trp Gly Ser Asp Tyr Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg
15 435 440 445

Pro Phe Gly Asn Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg
450 455 460

Thr Ser Gly Ser Leu Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly Ala
465 470 475 480

20 Tyr Gly Val Asp His Ala Ile Arg Ala Lys Lys Val Glu Asp Phe Leu
485 490 495

Lys Gly Lys Ser Leu Ser Ser Phe Val Ile Leu Glu Ala Ile Lys Leu
500 505 510

Leu Lys Asp Thr Val Ser Pro Ser Glu Gly Thr Thr His His Glu Tyr
25 515 520 525

Arg Val Ser Leu Ala Val Ser Phe Leu Phe Ser Phe Leu Ser Ser Leu
530 535 540

Ala Asn Ser Ser Ser Ala Pro Ser Asn Ile Asp Thr Pro Asn Gly Ser
545 550 555 560

5 Tyr Thr His Glu Thr Gly Ser Asn Val Asp Ser Pro Glu Arg His Ile
565 570 575

Lys Val Asp Ser Asn Asp Leu Pro Ile Arg Ser Arg Gln Glu Met Val
580 585 590

Phe Ser Asp Glu Tyr Lys Pro Val Gly Lys Pro Ile Lys Lys Val Gly
595 600 605

Ala Glu Ile Gln Ala Ser Gly Glu Ala Val Tyr Val Asp Asp Ile Pro
610 615 620

Ala Pro Lys Asp Cys Leu Tyr Gly Ala Phe Ile Tyr Ser Thr His Pro
625 630 635 640

15 His Ala His Val Arg Ser Ile Asn Phe Lys Ser Ser Leu Ala Ser Gln
645 650 655

Lys Val Ile Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Glu
660 665 670

Asn Ile Gly Ser Ser Phe Leu Met Gln Gly Glu Ala Leu Phe Ala Asp
675 680 685

Pro Ile Ala Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Glu
690 695 700

705 710 715 720

25 Ser Thr Glu Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile

725 730 735

Gln Arg Asn Ser Tyr Ile Gln Ile Pro Pro Phe Leu Ala Pro Lys Pro

740 745 750

Val Gly Asp Tyr Asn Lys Gly Met Ala Glu Ala Asp His Lys Ile Leu

5 755 760 765

Ser Ala Glu Val Lys Leu Glu Ser Gln Tyr Tyr Phe Tyr Met Glu Thr

770 775 780

Gln Ala Ala Leu Ala Ile Pro Asp Glu Asp Asn Cys Ile Thr Ile Tyr

785 790 795 800

10 Ser Ser Thr Gln Met Pro Glu Leu Thr Gln Asn Leu Ile Ala Arg Cys

 805 810 815

Leu Gly Ile Pro Phe His Asn Val Arg Val Ile Ser Arg Arg Val Gly

 820 825 830

Gly Gly Phe Gly Gly Lys Ala Met Lys Ala Thr His Thr Ala Cys Ala

15 835 840 845

Cys Ala Leu Ala Ala Phe Lys Leu Arg Arg Pro Val Arg Met Tyr Leu

 850 855 860

Asp Arg Lys Thr Asp Met Ile Met Ala Gly Gly Arg His Pro Met Lys

865 870 875 880

20 Ala Lys Tyr Ser Val Gly Phe Lys Ser Asp Gly Lys Ile Thr Ala Leu

 885 890 895

His Leu Asp Leu Gly Ile Asn Ala Gly Ile Ser Pro Asp Val Ser Pro

 900 905 910

Leu Met Pro Arg Ala Ile Ile Gly Ala Leu Lys Lys Tyr Asn Trp Gly

25 915 920 925

Thr Leu Glu Phe Asp Thr Lys Val Cys Lys Thr Asn Val Ser Ser Lys
930 935 940

Ser Ala Met Arg Ala Pro Gly Asp Val Gln Gly Ser Phe Ile Ala Glu
945 950 955 960

5 Ala Ile Ile Glu His Val Ala Ser Ala Leu Ala Leu Asp Thr Asn Thr
965 970 975

Val Arg Arg Lys Asn Leu His Asp Phe Glu Ser Leu Glu Val Phe Tyr
980 985 990

Gly Glu Ser Ala Gly Glu Ala Ser Thr Tyr Ser Leu Val Ser Met Phe
10 995 1000 1005

Asp Lys Leu Ala Leu Ser Pro Glu Tyr Gln His Arg Ala Ala Met Ile
1010 1015 1020

Glu Gln Phe Asn Ser Ser Asn Lys Trp Lys Lys Arg Gly Ile Ser Cys
1025 1030 1035 1040

15 Val Pro Ala Thr Tyr Glu Val Asn Leu Arg Pro Thr Pro Gly Lys Val
1045 1050 1055

Ser Ile Met Asn Asp Gly Ser Ile Ala Val Glu Val Gly Ile Glu
1060 1065 1070

Ile Gly Gln Gly Leu Trp Thr Lys Val Lys Gln Met Thr Ala Phe Gly
20 1075 1080 1085

Leu Gly Gln Leu Cys Pro Asp Gly Gly Glu Cys Leu Leu Asp Lys Val
1090 1095 1100

Arg Val Ile Gln Ala Asp Thr Leu Ser Leu Ile Gln Gly Gly Met Thr
1105 1110 1115 1120

25 Ala Gly Ser Thr Thr Ser Glu Thr Ser Cys Glu Thr Val Arg Gln Ser

1125 1130 1135

Cys Val Ala Leu Val Glu Lys Leu Asn Pro Ile Lys Glu Ser Leu Glu

1140 1145 1150

Ala Lys Ser Asn Thr Val Glu Trp Ser Ala Leu Ile Ala Gln Ala Ser

5 1155 1160 1165

Met Ala Ser Val Asn Leu Ser Ala Gln Pro Tyr Trp Thr Pro Asp Pro

1170 1175 1180

Ser Phe Lys Ser Tyr Leu Asn Tyr Gly Ala Gly Thr Ser Glu Val Glu

1185 1190 1195 1200

10 Val Asp Ile Leu Thr Gly Ala Thr Thr Ile Leu Arg Ser Asp Leu Val

1205 1210 1215

Tyr Asp Cys Gly Gln Ser Leu Asn Pro Ala Val Asp Leu Gly Gln Ile

1220 1225 1230

Glu Gly Cys Phe Val Gln Gly Ile Gly Phe Phe Thr Asn Glu Asp Tyr

15 1235 1240 1245

Lys Thr Asn Ser Asp Gly Leu Val Ile His Asp Gly Thr Trp Thr Tyr

1250 1255 1260

Lys Ile Pro Thr Val Asp Asn Ile Pro Lys Glu Phe Asn Val Glu Met

1265 1270 1275 1280

20 Phe Asn Ser Ala Pro Asp Lys Lys Arg Val Leu Ser Ser Lys Ala Ser

1285 1290 1295

Gly Glu Pro Pro Leu Val Leu Ala Thr Ser Val His Cys Ala Met Arg

1300 1305 1310

Glu Ala Ile Arg Ala Ala Arg Lys Glu Phe Ser Val Ser Thr Ser Pro

25 1315 1320 1325

Ala Lys Ser Ala Val Thr Phe Gln Met Asp Val Pro Ala Thr Met Pro

1330

1335

1340

Val Val Lys Glu Leu Cys Gly Leu Asp Val Val Glu Arg Tyr Leu Glu

1345

1350

1355

5 Asn Val Ser Ala Ala Ser Ala Gly Pro Asn Thr Ala Lys Ala

SEQ ID NO: 2

SEQUENCE LENGTH: 4,412

SEQUENCE TYPE: Nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays L.*)

10 STRAIN: cultivar: Golden Cross Bantam 70

FEATURES OF SEQUENCE:

KEY: CDS

LOCATION: 46..4120 (including termination codon)

IDENTIFICATION METHOD: E

15 SEQUENCE DESCRIPTION

GTG CTG TGT TGT GCT GTG CTG CGT GCT GTG GAG GGG GAG GAG GAG ATG 48

GGG AAG GAG GCA GGG GCA GCG GAG TCG TCG ACG GTG GTG CTG GCC GTC 96

AAC GGC AAG CGC TAC GAG GCG GCC GGC GTG GCT CCG TCC ACG TCG CTG 144

CTG GAG TTC CTC CGC ACC CAG ACG CCC GTC AGA GGC CCC AAG CTC GGC 192

20 TGC GGC GAA GGT GGC TGC GGT GCA TGC GTG GTC CTC GTC TCC AAG TAC 240

GAC CCG GCC ACG GAC GAG GTG ACC GAG TTC TCT GCC AGC TCC TGC CTG 288

ACG CTG CTC CAC AGC GTG GAC CGC TGC TCA GTG ACC ACC AGC GAG GGA 336

ATC GGC AAC ACC AGG GAT GGC TAC CAC CCC GTG CAG CAG CGC CTC TCC 384

GGC TTC CAC GCC TCG CAG TGC GGC TTC TGC ACA CCC GGC ATG TGC ATG 432

25 TCC ATC TTC TCC GCC CTT GTC AAG GCC GAC AAC AAG TCC GAT CGC CCG 480

	GAC CCT CCT GCT GGC TTC TCC AAG ATC ACT ACC TCG GAG GCA GAG AAG	528
	GCT GTC TCG GGC AAC CTT TGT CGT TGC ACC GGA TAC AGA CCC ATT GTT	576
	GAC ACC TGC AAA AGC TTT GCC TCT GAT GTT GAC CTC GAG GAC CTA GGC	624
	CTC AAC TGT TTC TGG AAG AAG GGC GAA GAA CCT GCA GAA GTC AGC AGG	672
5	CTG CCG GGG TAC AAC AGC GGT GCC GTC TGC ACC TTT CCA GAG TTT CTC	720
	AAA TCC GAA ATC AAG TCT ACT ATG AAG CAG GTG AAC GAT GTC CCC ATT	768
	GCA GCC TCA GGT GAT GGC TGG TAC CAT CCT AAG AGC ATT GAA GAG CTT	816
	CAC AGG TTG TTT GAT TCC AGC TGG TTT GAT GAC AGT TCT GTG AAG ATT	864
	GTT GCT TCA AAC ACT GGG TCT GGA GTG TAC AAG GAT CAG GAC CTC TAC	912
10	GAC AAG TAC ATT GAC ATC AAA GGA ATC CCA GAG CTT TCA GTC ATC AAT	960
	AAA AAC GAC AAA GCA ATT GAG CTT GGA TCA GTT GTG TCC ATC TCT AAA	1008
	GCT ATT GAA GTG CTG TCA GAT GGA AAT TTG GTC TTC AGA AAG ATT GCT	1056
	GAT CAC CTC AAC AAA GTG GCT TCA CCG TTT GTT CGG AAC ACT GCA ACC	1104
	ATA GGA GGA AAC ATA ATG ATG GCA CAA AGG TTG CCA TTT GAA TCG GAT	1152
15	GTT GCA ACC GTG CTC CTA GCT GCG GGT TCG ACA GTC ACA GTC CAG GTG	1200
	GCT TCC AAA AGG CTG TGC TTC ACT CTG GAG GAA TTC TTG GAA CAA CCT	1248
	CCA TGT GAT TCT AGG ACC CTG CTG CTG AGC ATA TTT ATC CCA GAA TGG	1296
	GGT TCA GAC TAT GTC ACC TTT GAG ACT TTC CGA GCC GCC CCA CGA CCA	1344
	TTT GGA AAT GCT GTC TCT TAT GTA AAC TCT GCT TTC TTG GCA AGG ACA	1392
20	TCA GGC AGC CTT CTA ATT GAG GAT ATA TGC TTG GCA TTT GGT GCC TAC	1440
	GGA GTC GAT CAT GCC ATC AGA GCT AAG AAG GTT GAA GAT TTC TTG AAG	1488
	GGA AAA TCG CTG AGC TCA TTT GTG ATA CTT GAA GCA ATT AAA CTA CTC	1536
	AAA GAT ACC GTT TCA CCA TCA GAA GGC ACT ACA CAT CAT GAA TAC AGG	1584
	GTC AGC TTG GCT GTC AGT TTC TTG TTC AGT TTC TTA TCT TCC CTT GCC	1632
25	AAC AGT TCG AGT GCA CCA TCA AAT ATT GAT ACT CCC AAT GGG TCA TAT	1680

	ACT CAT GAA ACT GGT AGC AAT GTG GAC TCA CCT GAG AGG CAT ATT AAG	1728
	GTT GAC AGC AAT GAT TTG CCA ATT CGT TCA AGA CAA GAA ATG GTT TTC	1776
	AGC GAT GAG TAC AAG CCT GTT GGC AAG CCG ATC AAG AAA GTC GGG GCA	1824
	GAG ATC CAA GCA TCA GGG GAG GCT GTG TAC GTT GAT GAT ATC CCT GCT	1872
5	CCC AAG GAT TGC CTC TAT GGA GCA TTT ATC TAC AGC ACA CAT CCT CAT	1920
	GCT CAT GTG AGA AGT ATC AAC TTC AAA TCA TCC TTG GCT TCA CAG AAG	1968
	GTC ATC ACA GTT ATA ACC GCA AAG GAT ATT CCA AGC GGT GGA GAA AAT	2016
	ATT GGA AGC AGC TTC CTG ATG CAA GGA GAA GCA CTA TTT GCA GAT CCA	2064
	ATC GCT GAA TTT GCT GGT CAA AAT ATT GGT GTC GTG ATT GCT GAA ACA	2112
10	CAA AGA TAT GCT AAT ATG GCT GCA AAG CAA GCT GTT GTT GAG TAT AGC	2160
	ACA GAA AAT CTG CAG CCA CCA ATT CTG ACA ATA GAA GAT GCC ATC CAA	2208
	AGA AAC AGC TAC ATC CAA ATT CCC CCA TTT TTA GCT CCA AAG CCA GTT	2256
	GGT GAC TAC AAC AAA GGG ATG GCT GAA GCA GAC CAC AAG ATT CTA TCA	2304
	GCA GAG GTA AAA CTT GAA TCC CAG TAC TAC TTC TAC ATG GAA ACT CAA	2352
15	GCA GCA CTA GCG ATT CCT GAT GAA GAT AAC TGC ATA ACA ATC TAT TCC	2400
	TCG ACA CAA ATG CCT GAG CTC ACA CAA AAT TTG ATA GCA AGG TGT CTT	2448
	GGC ATT CCA TTT CAC AAT GTC CGT GTC ATC AGC AGA AGA GTA GGA GGA	2496
	GGC TTT GGT GGA AAG GCA ATG AAA GCA ACG CAT ACT GCA TGT GCA TGT	2544
	GCC CTT GCT GCC TTC AAG CTG CGG CGT CCA GTT AGG ATG TAC CTC GAT	2592
20	CGC AAG ACG GAC ATG ATA ATG GCT GGA GGG AGA CAT CCA ATG AAG GCG	2640
	AAG TAC TCT GTT GGG TTC AAG TCA GAT GGC AAG ATC ACA GCC TTG CAC	2688
	CTA GAT CTT GGA ATC AAT GCT GGA ATA TCA CCA GAT GTG AGT CCA TTG	2736
	ATG CCA CGT GCT ATC ATA GGA GCT CTC AAA AAG TAC AAC TGG GGC ACT	2784
	CTT GAA TTT GAC ACC AAG GTC TGC AAG ACA AAT GTC TCA TCA AAG TCA	2832
25	GCA ATG CGA GCT CCT GGA GAT GTG CAG GGC TCT TTC ATC GCT GAA GCC	2880

	ATC ATC GAG CAT GTT GCC TCA GCA CTC GCA CTA GAC ACT AAC ACC GTC	2928
	AGG AGG AAG AAC CTT CAT GAT TTT GAA AGC CTT GAA GTT TTC TAT GGA	2976
	GAA AGT GCA GGT GAA GCT TCT ACA TAC AGC CTG GTT TCC ATG TTT GAC	3024
	AAG CTG GCC TTG TCT CCA GAA TAC CAG CAC AGG GCT GCA ATG ATT GAG	3072
5	CAG TTC AAT AGC AGC AAC AAA TGG AAG AAA CGC GGC ATT TCT TGT GTG	3120
	CCA GCC ACT TAT GAG GTT AAT CTT CGA CCA ACT CCA GGC AAG GTG TCA	3168
	ATC ATG AAT GAT GGT TCC ATC GCT GTC GAG GTT GGA GGA ATT GAG ATA	3216
	GGT CAA GGA TTG TGG ACT AAA GTG AAG CAG ATG ACG GCC TTT GGA CTG	3264
	GGA CAG CTG TGT CCT GAT GGT GGC GAA TGC CTT CTG GAC AAG GTT CGG	3312
10	GTT ATC CAG GCA GAC ACA TTA AGC CTG ATC CAA GGA GGT ATG ACT GCT	3360
	GGG AGC ACC ACT TCT GAA ACT AGC TGT GAA ACA GTT CGG CAA TCT TGT	3408
	GTT GCA CTG GTT GAG AAG CTG AAC CCT ATC AAG GAG AGT CTC GAA GCT	3456
	AAG TCC AAC ACA GTG GAA TGG AGT GCC TTG ATT GCT CAG GCA AGC ATG	3504
	GCG AGT GTG AAC CTA TCA GCA CAG CCG TAC TGG ACT CCT GAT CCA TCT	3552
15	TTC AAG AGC TAC TTG AAC TAC GGA GCT GGC ACC AGT GAG GTG GAA GTT	3600
	GAT ATC CTA ACA GGA GCA ACC ACA ATT CTG CGA AGC GAC CTG GTG TAT	3648
	GAC TGC GGG CAG AGC CTA AAC CCT GCT GTA GAC TTG GGC CAG ATC GAG	3696
	GGC TGC TTT GTC CAA GGA ATA GGG TTC TTC ACG AAC GAG GAC TAC AAG	3744
	ACG AAT TCC GAC GGG TTG GTC ATC CAC GAC GGC ACA TGG ACG TAC AAG	3792
20	ATC CCC ACG GTG GAT AAT ATC CCG AAG GAG TTC AAT GTT GAG ATG TTT	3840
	AAC AGC GCC CCT GAC AAG AAG CGT GTC CTA TCT TCC AAA GCG TCG GGC	3888
	GAG CCG CCG CTG GTT CTC GCA ACC TCG GTG CAC TGC GCG ATG AGG GAG	3936
	GCC ATC AGG GCG GCG AGG AAG GAG TTC TCG GTC AGC ACC AGC CCC GCG	3984
	AAA TCC GCC GTC ACA TTC CAG ATG GAC GTG CCG GCG ACG ATG CCT GTC	4032
25	GTC AAG GAG CTC TGC GGC CTC GAC GTC GTG GAG AGG TAC CTC GAG AAC	4080

GTG TCT GCC GCC AGT GCC GGC CCA AAC ACA GCG AAA GCA TAG ATC CAG 4128
CAG GCC TCA GGG TGC AGT CGG CGC ACT GCC AGA GAT GAT GTG TGC TGC 4176
CCT GAT GTA CAG ACA GTA CAG TAC AGA GGA GAG AGA ATT GGG GGA ACT 4224
CAG GAA CTG CGA GGA GCG ATG AAC AGT ATA TAG AGT GAA AAA TAA AAG 4272
5 TGC TTC GTA CTA ATA ATC ACT AGA AAA AAT TAT GCA CAT CTC CCA CGC 4320
ACT ACC GGC ACG ACT GTT GAA TAT TTT GTA AAA TAA GAT GTC ATA AGC 4368
TAT TTA TTT TCT GTA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA 4412

SEQ ID NO: 3

SEQUENCE LENGTH: 1,349

SEQUENCE TYPE: Amino acid

5 TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays L.*)

STRAIN: cultivar: Golden Cross Bantam 70

10 SEQUENCE DESCRIPTION

5 10 15

Met Glu Met Gly Lys Ala Ala Ala Val Val Leu Ala Val Asn Gly Lys

20 25 30

Arg Tyr Glu Ala Ala Gly Val Asp Pro Ser Thr Thr Leu Leu Glu Phe

15 35 40 45

Leu Arg Thr His Thr Pro Val Arg Gly Pro Lys Leu Gly Cys Gly Glu

50 55 60

Gly Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys Tyr Asp Pro Ala

65 70 75 80

20 Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys Leu Thr Leu Leu

85 90 95

His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu Gly Ile Gly Asn

100 105 110

Thr Lys Asp Gly Tyr His Pro Val Gln Gln Arg Leu Ser Gly Phe His

25 115 120 125

Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys Met Ser Ile Phe
130 135 140

Ser Ala Leu Val Lys Ala Asp Lys Ala Ala Asn Arg Pro Ala Pro Pro
145 150 155 160

5 Ala Gly Phe Ser Lys Leu Thr Ser Ser Glu Ala Glu Lys Ala Val Ser
165 170 175

Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile Val Asp Ala Cys
180 185 190

Lys Ser Phe Ala Ala Asp Val Asp Leu Glu Asp Leu Gly Leu Asn Cys
10 195 200 205

Phe Trp Lys Lys Gly Asp Glu Pro Ala Asp Val Ser Lys Leu Pro Gly
210 215 220

Tyr Asn Ser Gly Asp Val Cys Thr Phe Pro Asp Phe Leu Lys Ser Glu
225 230 235 240

15 Met Lys Ser Ser Ile Gln Gln Ala Asn Ser Ala Pro Val Pro Val Ser
245 250 255

Asp Asp Gly Trp Tyr Arg Pro Arg Ser Ile Asp Glu Leu His Arg Leu
260 265 270

Phe Gln Ser Ser Ser Phe Asp Glu Asn Ser Val Lys Ile Val Ala Ser
20 275 280 285

Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu Tyr Asp Lys Tyr
290 295 300

Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile Asn Arg Asn Asp
305 310 315 320

25 Lys Gly Ile Glu Leu Gly Ser Val Val Ser Ile Ser Lys Ala Ile Glu

325 330 335

Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile Ala Gly His Leu
340 345 350

Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala Thr Ile Gly Gly
5 355 360 365

Asn Ile Val Met Ala Gln Arg Leu Pro Phe Ala Ser Asp Ile Ala Thr
370 375 380

Ile Leu Leu Ala Ala Gly Ser Thr Val Thr Ile Gln Val Ala Ser Lys
385 390 395 400

10 Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Gln Gln Pro Pro Cys Asp
405 410 415

Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu Trp Gly Ser Asn
420 425 430

Asp Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg Pro Leu Gly Asn
435 440 445

Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg Thr Ser Leu Asp
450 455 460

Ala Ala Ser Lys Asp His Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly
465 470 475 480

20 Ala Tyr Gly Ala Asp His Ala Ile Arg Ala Arg Lys Val Glu Asp Tyr
485 490 495

Leu Lys Gly Lys Thr Val Ser Ser Val Ile Leu Glu Ala Val Arg
500 505 510

Leu Leu Lys Gly Ser Ile Lys Pro Ser Glu Gly Ser Thr His Pro Glu
25 515 520 525

Tyr Arg Ile Ser Leu Ala Val Ser Phe Leu Phe Thr Phe Leu Ser Ser
530 535 540

Leu Ala Asn Ser Leu Asn Glu Ser Ala Lys Val Ser Gly Thr Asn Glu
545 550 555 560

5 His Ser Pro Glu Lys Gln Leu Lys Leu Asp Ile Asn Asp Leu Pro Ile
565 570 575

Arg Ser Arg Gln Glu Ile Phe Phe Thr Asp Ala Tyr Lys Pro Val Gly
580 585 590

Lys Ala Ile Lys Lys Ala Gly Val Glu Ile Gln Ala Ser Gly Glu Ala
10 595 600 605

Val Tyr Val Asp Asp Ile Pro Ala Pro Lys Asp Cys Leu Tyr Gly Ala
610 615 620

Phe Ile Tyr Ser Thr His Pro His Ala His Val Lys Ser Ile Asn Phe
625 630 635 640

15 Lys Pro Ser Leu Ala Ser Gln Lys Ile Ile Thr Val Ile Thr Ala Lys
645 650 655

Asp Ile Pro Ser Gly Gly Gln Asn Val Gly Tyr Ser Phe Pro Met Ile
660 665 670

Gly Glu Glu Ala Leu Phe Ala Asp Pro Val Ala Glu Phe Ala Gly Gln
20 675 680 685

Asn Ile Gly Val Val Ile Ala Gln Thr Gln Lys Tyr Ala Tyr Met Ala
690 695 700

Ala Lys Gln Ala Ile Ile Glu Tyr Ser Thr Glu Asn Leu Gln Pro Pro
705 710 715 720

25 Ile Leu Thr Ile Glu Asp Ala Ile Glu Arg Ser Ser Phe Phe Gln Thr

725 730 735

Leu Pro Phe Val Ala Pro Lys Pro Val Gly Asp Tyr Asp Lys Gly Met

740 745 750

Ser Glu Ala Asp His Lys Ile Leu Ser Ala Glu Val Lys Ile Glu Ser

5 755 760 765

Gln Tyr Phe Phe Tyr Met Glu Pro Gln Val Ala Leu Ala Ile Pro Asp

770 775 780

Glu Asp Asn Cys Ile Thr Ile Tyr Phe Ser Thr Gln Leu Pro Glu Ser

785 790 795 800

10 Thr Gln Asn Val Val Ala Lys Cys Val Gly Ile Pro Phe His Asn Val

 805 810 815

Arg Val Ile Thr Arg Arg Val Gly Gly Gly Phe Gly Gly Lys Ala Leu

 820 825 830

Lys Ser Met His Val Ala Cys Ala Cys Ala Val Ala Ala Leu Lys Leu

15 835 840 845

Gln Arg Pro Val Arg Met Tyr Leu Asp Arg Lys Thr Asp Met Ile Met

 850 855 860

Ala Gly Gly Arg His Pro Met Lys Val Lys Tyr Ser Val Gly Phe Lys

865 870 875 880

20 Ser Asn Gly Lys Ile Thr Ala Leu His Leu Asp Leu Gly Ile Asn Gly

 885 890 895

Gly Ile Ser Pro Asp Met Ser Pro Met Ile Ala Ala Pro Val Ile Gly

 900 905 910

Ser Leu Lys Lys Tyr Asn Trp Gly Asn Leu Ala Phe Asp Thr Lys Val

25 915 920 925

Cys Lys Thr Asn Val Ser Ser Lys Ser Ser Met Arg Ala Pro Gly Asp

930 935 940

Ala Gln Gly Ser Phe Ile Ala Glu Ala Ile Ile Glu His Val Ala Ser

945 950 955 960

5 Ala Leu Ser Ala Asp Thr Asn Thr Ile Arg Arg Lys Asn Leu His Asp

965 970 975

Phe Glu Ser Leu Ala Val Phe Phe Gly Asp Ser Ala Gly Glu Ala Ser

980 985 990

Thr Tyr Ser Leu Val Thr Met Phe Asp Lys Leu Ala Ser Ser Pro Glu

10 995 1000 1005

Tyr Gln His Arg Ala Glu Met Val Glu Gln Phe Asn Arg Ser Asn Lys

1010 1015 1020

Trp Lys Lys Arg Gly Ile Ser Cys Val Pro Val Thr Tyr Glu Val Gln

1025 1030 1035 1040

15 Leu Arg Pro Thr Pro Gly Lys Val Ser Ile Met Asn Asp Gly Ser Ile

1045 1050 1055

Ala Val Glu Val Gly Val Glu Leu Gly Gln Gly Leu Trp Thr Lys

1060 1065 1070

Val Lys Gln Met Thr Ala Phe Gly Leu Gly Gln Leu Cys Pro Gly Gly

20 1075 1080 1085

Gly Glu Ser Leu Leu Asp Lys Val Arg Val Ile Gln Ala Asp Thr Leu

1090 1095 1100

Ser Met Ile Gln Gly Gly Val Thr Gly Gly Ser Thr Thr Ser Glu Thr

1105 1110 1115 1120

25 Ser Cys Glu Ala Val Arg Lys Ser Cys Val Ala Leu Val Glu Ser Leu

1125 1130 1135

Lys Pro Ile Lys Glu Asn Leu Glu Ala Lys Thr Gly Thr Val Glu Trp

1140 1145 1150

Ser Ala Leu Ile Ala Gln Ala Ser Met Ala Ser Val Asn Leu Ser Ala

5 1155 1160 1165

His Ala Tyr Trp Thr Pro Asp Pro Thr Phe Thr Ser Tyr Leu Asn Tyr

1170 1175 1180

Gly Ala Gly Thr Ser Glu Val Glu Ile Asp Val Leu Thr Gly Ala Thr

1185 1190 1195 1200

10 Thr Ile Leu Arg Ser Asp Leu Val Tyr Asp Cys Gly Gln Ser Leu Asn

1205 1210 1215

Pro Ala Val Asp Leu Gly Gln Val Glu Gly Ala Phe Val Gln Gly Val

1220 1225 1230

Gly Phe Phe Thr Asn Glu Glu Tyr Ala Thr Asn Ser Asp Gly Leu Val

15 1235 1240 1245

Ile His Asp Gly Thr Trp Thr Tyr Lys Ile Pro Thr Val Asp Thr Ile

1250 1255 1260

Pro Lys Gln Phe Asn Val Glu Leu Ile Asn Ser Ala Arg Asp Gln Lys

1265 1270 1275 1280

20 Arg Val Leu Ser Ser Lys Ala Ser Gly Glu Pro Pro Leu Leu Leu Ala

1285 1290 1295

Ser Ser Val His Cys Ala Met Arg Glu Ala Ile Arg Ala Ala Arg Lys

1300 1305 1310

Glu Phe Ser Val Cys Thr Gly Pro Ala Asn Ser Ala Ile Thr Phe Gln

25 1315 1320 1325

Met Asp Val Pro Ala Thr Met Pro Val Val Lys Glu Leu Cys Gly Leu

1330

1335

1340

Asp Val Val Glu Arg Tyr Leu Glu Ser Val Ser Ala Ala Ser Pro Thr

1345

5 Asn Thr Ala Lys Ala

SEQ ID NO: 4

SEQUENCE LENGTH: 4,359

SEQUENCE TYPE: Nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays L.*)

10 STRAIN: cultivar: Golden Cross Bantam 70

FEATURES OF SEQUENCE:

KEY: CDS

LOCATION: 91..4138 (including termination codon)

IDENTIFICATION METHOD: E

15 SEQUENCE DESCRIPTION

CCG GCT CTC TCG GTG CAG ACG TCC GGG ACT AGT ACG TGG ATC GGG CCG	48
GGG GCA ACT CGA GTC GTC AAG AAG GCT GCT ACC TGC TAG AGG ATG GAG	96
ATG GGG AAG GCG GCG GTG GTG CTG GCG GTG AAC GGC AAG CGG TAC	144
GAG GCC GCC GGC GTG GAC CCG TCG ACG ACG CTG CTG GAG TTC CTG CGC	192
20 ACC CAC ACG CCC GTC AGG GGG CCC AAG CTC GGC TGC GGC GAA GGT GGC	240
TGC GGT GCA TGC GTT GTG CTT GTC TCG AAG TAC GAC CCA GCC ACC GAC	288
GAG GTG ACC GAG TTC TCA GCG AGC TCC TGC CTG ACG CTG CTC CAT AGC	336
GTG GAC CGC TGC TCG GTG ACC ACC AGC GAG GGC ATT GGC AAC ACC AAG	384
GAT GGC TAC CAC CCT GTG CAG CAG CGC CTC TCC GGC TTC CAC GCC TCC	432
25 CAG TGC GGT TTC TGC ACG CCC GGC ATG TGC ATG TCC ATC TTC TCT GCG	480

	CTT GTC AAA GCC GAC AAG GCG GCC AAC CGG CCA GCC CCA CCG GCC GGC	528
	TTC TCC AAG CTC ACT TCC TCG GAG GCT GAG AAG GCT GTC TCT GGC AAC	576
	CTG TGC CGC TGC ACA GGG TAC AGG CCC ATC GTC GAC GCC TGT AAG AGC	624
	TTC GCA GCC GAT GTT GAT CTT GAG GAC CTG GGC CTC AAC TGC TTC TGG	672
5	AAG AAG GGT GAT GAG CCT GCA GAT GTC AGC AAG CTG CCA GGC TAC AAC	720
	AGT GGT GAC GTC TGC ACT TTC CCT GAC TTT CTC AAA TCT GAG ATG AAG	768
	TCC TCA ATT CAG CAG GCT AAC AGC GCT CCA GTT CCT GTT TCT GAC GAC	816
	GGC TGG TAC CGT CCT AGG AGC ATT GAC GAG CTT CAC AGG TTG TTT CAA	864
	TCT AGC TCC TTC GAT GAA AAT TCC GTG AAG ATA GTG GCT TCA AAC ACT	912
10	GGG TCT GGA GTG TAC AAG GAT CAG GAC CTT TAT GAC AAG TAC ATT GAC	960
	ATC AAA GGA ATC CCA GAG CTT TCA GTC ATC AAC AGA AAC GAC AAA GGA	1008
	ATT GAG CTT GGA TCA GTT GTG TCC ATC TCT AAA GCT ATT GAG GTG CTG	1056
	TCA GAT GGA AAT CTC GTC TTC AGA AAG ATT GCT GGT CAC CTG AAC AAA	1104
	G TG GCT TCA CCG TTT GTT CCG AAC ACT GCA ACC ATA GGT GGA AAC ATA	1152
15	GTC ATG GCA CAA AGA TTG CCA TTC GCA TCG GAC ATT GCA ACC ATA CTA	1200
	CTA GCT GCA GGT TCA ACA GTC ACA ATC CAG GTG GCT TCC AAA AGG CTG	1248
	TGC TTC ACT CTG GAG GAG TTC TTG CAG CAG CCT CCA TGC GAT TCT AGG	1296
	ACC CTG CTG CTG AGC ATA TTT ATC CCG GAA TGG GGC TCA AAT GAT GTC	1344
	ACC TTT GAG ACT TTC CGA GCA GCA CCT CGT CCA CTT GGC AAT GCT GTC	1392
20	TCA TAT GTC AAT TCA GCT TTC TTG GCA AGG ACT TCA TTG GAT GCA GCA	1440
	TCA AAG GAC CAT CTC ATC GAG GAT ATA TGT CTG GCG TTC GGT GCT TAT	1488
	GGA GCT GAT CAT GCT ATT AGA GCT AGA AAG GTT GAG GAT TAC CTG AAG	1536
	GGC AAA ACA GTG AGC TCG TCT GTC ATA CTT GAA GCT GTT CGG TTG CTT	1584
	AAA GGG TCT ATT AAA CCA TCA GAA GGC TCA ACA CAT CCT GAG TAT AGA	1632
25	ATT AGC TTG GCT GTC AGT TTC TTG TTT ACC TTC CTA TCC TCC CTT GCC	1680

	AAC AGC TTG AAT GAA TCT GCA AAG GTT AGT GGT ACC AAC GAG CAC TCA	1728
	CCA GAG AAG CAA CTC AAG TTG GAC ATC AAT GAT TTG CCA ATA CGA TCA	1776
	AGA CAA GAA ATA TTT TTC ACT GAT GCA TAT AAG CCA GTT GGC AAA GCA	1824
	ATT AAG AAA GCT GGG GTA GAG ATC CAA GCT TCA GGG GAA GCT GTG TAC	1872
5	GTT GAT GAT ATC CCT GCT CCC AAA GAT TGC CTC TAT GGG GCA TTT ATT	1920
	TAT AGC ACA CAC CCT CAT GCA CAT GTA AAG TCA ATC AAC TTT AAA CCA	1968
	TCT TTG GCT TCA CAG AAG ATC ATC ACA GTT ATC ACT GCA AAG GAT ATT	2016
	CCC AGC GGT GGA CAA AAT GTT GGT TAT AGC TTC CCG ATG ATT GGA GAA	2064
	GAA GCA CTT TTT GCA GAT CCA GTT GCT GAA TTT GCT GGT CAA AAT ATT	2112
10	GGT GTC GTG ATT GCT CAA ACA CAG AAG TAT GCC TAC ATG GCG GCA AAG	2160
	CAA GCC ATC ATT GAG TAT AGC ACA GAA AAT CTG CAG CCA CCA ATT CTG	2208
	ACA ATA GAA GAT GCA ATT GAA CGA AGC AGC TTC TTC CAA ACC CTC CCA	2256
	TTT GTA GCT CCT AAG CCA GTT GGT GAT TAC GAC AAA GGG ATG TCT GAA	2304
	GCT GAT CAC AAG ATT TTA TCG GCA GAG GTA AAA ATT GAA TCC CAA TAC	2352
15	TTT TTC TAC ATG GAG CCA CAA GTG GCG CTA GCT ATT CCT GAT GAA GAT	2400
	AAC TGC ATA ACC ATC TAT TTT TCG ACA CAA TTA CCT GAG TCC ACA CAA	2448
	AAT GTG GTT GCA AAG TGC GTT GGC ATT CCA TTT CAC AAT GTC CGT GTA	2496
	ATC ACC AGA AGG GTC GGA GGA GGC TTT GGT GGA AAA GCA TTG AAA TCA	2544
	ATG CAT GTT GCA TGT GCA GTT GCT GCA TTG AAG CTA CAA CGT	2592
20	CCA GTT CGG ATG TAC CTC GAT CGC AAG ACA GAC ATG ATA ATG GCA GGC	2640
	GGG CGG CAT CCT ATG AAG GTG AAG TAC TCT GTT GGG TTC AAG TCA AAC	2688
	GGC AAG ATC ACA GCC TTA CAT CTT GAT CTT GGG ATC AAT GGT GGA ATA	2736
	TCT CCA GAT ATG AGT CCA ATG ATT GCA GCA CCT GTC ATA GGT TCT CTC	2784
	AAA AAG TAC AAC TGG GGC AAT CTT GCA TTT GAC ACC AAG GTC TGC AAA	2832
25	ACA AAT GTC TCA TCA AAA TCG TCA ATG AGA GCT CCT GGA GAT GCG CAG	2880

	GGC TCT TTC ATT GCT GAA GCC ATC ATC GAG CAT GTT GCC TCG GCA CTT	2928
	TCA GCC GAC ACT AAT ACC ATA AGG AGA AAG AAC CTT CAT GAC TTT GAG	2976
	AGC CTT GCA GTG TTC TTT GGA GAT AGT GCA GGT GAA GCT TCT ACA TAC	3024
	AGC CTT GTC ACC ATG TTC GAT AAA TTG GCC TCC TCT CCA GAA TAC CAG	3072
5	CAC CGA GCT GAA ATG GTG GAA CAA TTC AAC CGA AGC AAC AAG TGG AAG	3120
	AAG CGT GGC ATT TCT TGT GTG CCT GTA ACA TAT GAG GTG CAG CTT CGG	3168
	CCA ACT CCA GGA AAG GTG TCT ATC ATG AAT GAT GGT TCC ATT GCT GTT	3216
	GAG GTT GGA GGG GTT GAG CTA GGC CAA GGG TTG TGG ACA AAA GTG AAG	3264
	CAG ATG ACG GCA TTC GGA CTA GGA CAG CTG TGT CCT GGC GGC GGT GAA	3312
10	AGC CTT CTA GAC AAG GTG CGG GTC ATC CAG GCC GAC ACA TTG AGC ATG	3360
	ATC CAA GGA GGG GTC ACT GGT GGG AGC ACC ACT TCT GAA ACT AGC TGT	3408
	GAA GCA GTT CGT AAG TCG TGT GTT GCA CTC GTC GAG AGC TTG AAG CCA	3456
	ATC AAG GAG AAT CTG GAG GCT AAA ACT GGC ACA GTG GAA TGG AGT GCC	3504
	TTG ATT GCA CAG GCA AGT ATG GCG AGC GTT AAC TTA TCG GCA CAT GCA	3552
15	TAC TGG ACC CCT GAT CCA ACT TTC ACA AGC TAT TTG AAC TAC GGA GCC	3600
	GGC ACT AGC GAG GTG GAA ATT GAT GTC CTG ACA GGA GCA ACA ACA ATT	3648
	CTA AGG AGT GAC CTT GTC TAC GAT TGC GGG CAA AGC TTG AAC CCT GCT	3696
	GTC GAT TTG GGG CAG GTG GAA GGT GCA TTC GTA CAA GGA GTA GGC TTC	3744
	TTC ACA AAC GAG GAG TAC GCA ACC AAC TCT GAC GGG TTG GTC ATC CAC	3792
20	GAT GGC ACA TGG ACG TAC AAG ATC CCC ACG GTC GAC ACC ATC CCA AAG	3840
	CAG TTC AAC GTT GAG CTG ATC AAC AGC GCC CGT GAC CAG AAG CGC GTC	3888
	CTC TCT TCC AAA GCA TCG GGC GAG CCT CCG CTT CTC CTA GCT TCC TCT	3936
	GTG CAC TGC GCA ATG AGG GAG GCC ATC AGG GCC GCC AGG AAA GAA TTC	3984
	TCG GTC TGC ACT GGT CCA GCG AAC TCC GCC ATC ACG TTC CAG ATG GAC	4032
25	GTG CCG GCA ACG ATG CCT GTC GTC AAG GAG CTC TGC GGC CTG GAT GTC	4080

GTT GAG AGG TAC CTG GAG AGC GTG TCG GCT GCC AGC CCA ACA AAC ACC 4128
GCT AAA GCA TAG ATC CAG TAG GCG CTC TAT CCA TGG TGT GAT GGC TTA 4176
ATC AAT CTG TAA AAC ACT AAG CGG CGT GAC ATG CCG AGC TTT CAG TGT 4224
TAG CTA TGA TGT ACA GAA GAA GAG GTA CCA ATG GCG AGT TGT GGC CAT 4272
5 GCG AAT CAG GAG TCA TGA ACC ATT GAG GGG GGA AAT AAA GTA AAT AAG 4320
TGT TGC GCC GGC GAA AAA 4359